

# SEQUENCE LISTING

<110> Duprat, Fabrice  
Lesage, Florian  
Fink, Michel  
Lazdunski, Michel

<120> FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING  
AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

<130> 1201-CIP-DIV-2-00

<141> 2001-08-24

<150> 09/144,914

<151> 1998-09-01

<150> 08/749,816

<151> 1996-11-15

<150> 60/095,234

<151> 1998-08-04

<150> FR 96/01565

<151> 1996-02-08

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<170> PatentIn Ver. 2.0

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Leu	Tyr	Leu	Val	Phe	Gly	Ala	Val	Val	Phe	Ser	Ser	Val	Glu	Leu	Pro	
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Leu	Glu	Glu	His	Glu	Cys	Leu	Ser	Glu	Gln	Gln	Leu	Glu	Gln	Phe	Leu	
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Gly	Arg	Val	Leu	Glu	Ala	Ser	Asn	Tyr	Gly	Val	Ser	Val	Leu	Ser	Asn	
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gcc	tcg	ggc	aac	tgg	aac	tgg	gac	ttc	acc	tcc	gcg	ctc	ttc	ttc	gcc	515
Ala	Ser	Gly	Asn	Trp	Asn	Trp	Asp	Phe	Thr	Ser	Ala	Leu	Phe	Phe	Ala	
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Phe	Thr	Leu	Leu	Phe	Leu	Thr	Ala	Val	Val	Gln	Arg	Ile	Thr	Val	His	
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Val	Thr	Arg	Arg	Pro	Val	Leu	Tyr	Phe	His	Ile	Arg	Trp	Gly	Phe	Ser	
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Lys	Gln	Val	Val	Ala	Ile	Val	His	Ala	Val	Leu	Leu	Gly	Phe	Val	Thr	
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Asp	Asp	Trp	Asn	Phe	Leu	Glu	Ser	Phe	Tyr	Phe	Cys	Phe	Ile	Ser	Leu	
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Gly	Leu	Ile	Ala	Met	Leu	Val	Val	Leu	Glu	Thr	Phe	Cys	Glu	Leu	His	
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Glu	Leu	Lys	Lys	Phe	Arg	Lys	Met	Phe	Tyr	Val	Lys	Lys	Asp	Lys	Asp	
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Ile Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu  
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cct ttt gtg gcc acc cag tca tct gcc tgc gtg gat ggc cct gca aac 1187  
Pro Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn  
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Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr  
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Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu  
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Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly  
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Leu	Lys	Lys	Phe	Arg	Lys	Met	Phe	Tyr	Val	Lys	Lys	Asp	Lys	Asp	Glu	
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Asp	Gln	Val	His	Ile	Ile	Glu	His	Asp	Gln	Leu	Ser	Phe	Ser	Ser	Ile	
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Thr	Asp	Gln	Ala	Ala	Gly	Met	Lys	Glu	Asp	Gln	Lys	Gln	Asn	Glu	Pro	
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ttc acc tac ctg ctg gtg ggc gcc gcg gtc ttc gac gcg ctg gag tcg 218

Phe Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser

20

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30

gag ccc gag ctg atc gag cgg cag cgg ctg gag ctg cgg cag cag gag 266

Glu Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu

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ctg cgg gcg cgc tac aac ctc agc cag ggc ggc tac gag gag ctg gag 314

Leu Arg Ala Arg Tyr Asn Leu Ser Gln Gly Gly Tyr Glu Glu Leu Glu

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cgc gtc gtg ctg cgc ctc aag ccg cac aag gcc ggc gtg cag tgg cgc 362

Arg Val Val Leu Arg Leu Lys Pro His Lys Ala Gly Val Gln Trp Arg

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70

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ttc gcc ggc tcc ttc tac ttc gcc atc acc gtc atc acc acc atc ggc 410

Phe Ala Gly Ser Phe Tyr Phe Ala Ile Thr Val Ile Thr Thr Ile Gly

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tac ggg cac gcg gca ccc agc acg gat ggc ggc aag gtg ttc tgc atg 458

Tyr Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met

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105

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ttc tac gcg ctg ctg ggc atc ccg ctc acg ctc gtc atg ttc cag agc 506

Phe Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser

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Leu Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala

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aag aag ggg ctg ggc atg cgg cgc gcc gac gtg tcc atg gcc aac atg 602

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gcc gcc ttc tcc cac tac gag cac tgg acc ttc ttc cag gcc tac tac 698

Ala Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr

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Tyr Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala

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Asn Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys	
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cgc gac gcc gag cac cgc gcg ctg ctc acg cgc aac ggg cag gcg ggc	938
Arg Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly	
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ggc ggc gga ggg ggt ggc agc gcg cac act acg gac acc gcc tca tcc	986
Gly Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser	
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Thr Ala Ala Ala Gly Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val	
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Leu His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu	
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aag ctg cag tac tcc atc ccc atg atc atc ccg cgg gac ctc tcc acg	1130
Lys Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr	
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Arg Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro	
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cgc tcc gcc atc agc tcg gtg tcc acg ggt ctg cac agc ctg tcc acc	1274
Arg Ser Ala Ile Ser Ser Val Ser Thr Gly Leu His Ser Leu Ser Thr	
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Phe Arg Gly Leu Met Lys Arg Arg Ser Ser Val	
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Lys	Gly	Leu	Gly	Met	Arg	Arg	Ala	Asp	Val	Ser	Met	Ala	Asn	Met	Val

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Leu Ile Gly Phe Phe Ser Cys Ile Ser Thr Leu Cys Ile Gly Ala Ala	165	170		175		
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Cys Phe Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr Val Ala Leu	195	200		205		
Gln Lys Asp Gln Ala Leu Gln Thr Gln Pro Gln Tyr Val Ala Phe Ser	210	215		220		
Phe Val Tyr Ile Leu Thr Gly Leu Thr Val Ile Gly Ala Phe Leu Asn	225	230		235		240
Leu Val Val Leu Arg Phe Met Thr Met Asn Ala Glu Asp Glu Lys Arg	245	250		255		
Asp Ala Glu His Arg Ala Leu Leu Thr Arg Asn Gly Gln Ala Gly Gly	260	265		270		
Gly Gly Gly Gly Gly Ser Ala His Thr Thr Asp Thr Ala Ser Ser Thr	275	280		285		
Ala Ala Ala Gly Gly Gly Gly Phe Arg Asn Val Tyr Ala Glu Val Leu	290	295		300		
His Phe Gln Ser Met Cys Ser Cys Leu Trp Tyr Lys Ser Arg Glu Lys	305	310		315		320
Leu Gln Tyr Ser Ile Pro Met Ile Ile Pro Arg Asp Leu Ser Thr Ser	325	330		335		
Asp Thr Cys Val Glu Gln Ser His Ser Ser Pro Gly Gly Gly Gly Arg	340	345		350		
Tyr Ser Asp Thr Pro Ser Arg Arg Cys Leu Cys Ser Gly Ala Pro Arg	355	360		365		
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Tyr	Tyr	Glu	Arg	Trp	Thr	Phe	Phe	Gln	Ala	Tyr	Tyr	Tyr	Cys	Phe	Ile
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Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp	Tyr	Val	Ala	Leu	Gln	Lys	Asp
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Gln	Ala	Leu	Gln	Thr	Gln	Pro	Gln	Tyr	Val	Ala	Phe	Ser	Phe	Val	Tyr
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Ile	Leu	Thr	Gly	Leu	Thr	Val	Ile	Gly	Ala	Phe	Leu	Asn	Leu	Val	Val
	225					230			235						240
Leu	Arg	Phe	Met	Thr	Met	Asn	Ala	Glu	Asp	Glu	Lys	Arg	Asp	Ala	Glu
			245						250					255	
His	Arg	Ala	Leu	Leu	Thr	His	Asn	Gly	Gln	Ala	Val	Gly	Leu	Gly	Gly
			260					265					270		
Leu	Ser	Cys	Leu	Ser	Gly	Ser	Leu	Gly	Asp	Val	Arg	Pro	Arg	Asp	Pro
		275					280					285			
Val	Thr	Cys	Ala	Ala	Ala	Ala	Gly	Gly	Val	Gly	Val	Gly	Val	Gly	Gly
	290					295					300				
Ser	Gly	Phe	Arg	Asn	Val	Tyr	Ala	Glu	Val	Leu	His	Phe	Gln	Ser	Met
	305					310					315				320
Cys	Ser	Cys	Leu	Trp	Tyr	Lys	Ser	Arg	Glu	Lys	Leu	Gln	Tyr	Ser	Ile
			325						330					335	
Pro	Met	Ile	Ile	Pro	Arg	Asp	Leu	Ser	Thr	Ser	Asp	Thr	Cys	Val	Glu
			340					345					350		

His Ser His Ser Ser Pro Gly Gly Gly Gly Arg Tyr Ser Asp Thr Pro  
 355 360 365

Ser His Pro Cys Leu Cys Ser Gly Thr Gln Arg Ser Ala Ile Ser Ser  
 370 375 380

Val Ser Thr Gly Leu His Ser Leu Ala Ala Phe Arg Gly Leu Met Lys  
 385 390 395 400

Arg Arg Ser Ser Val  
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<210> 6  
 <211> 347  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: TWIK-1 homolog

<400> 6

Met Tyr Thr Asp Glu Gly Glu Tyr Ser Gly Asp Thr Asp His Gly Gly  
 1 5 10 15

Ser Thr Met Gln Lys Met Ser Pro Asn Thr Arg Gln Asn Phe Arg Gln  
 20 25 30

Asn Val Asn Val Val Val Cys Leu Ser Ala Ala Ile Thr Leu Leu Val  
 35 40 45

Phe Asn Leu Ile Gly Ala Gly Ile Phe Tyr Leu Ala Glu Thr Gln Asn  
 50 55 60

Ser Ser Glu Ser Leu Asn Glu Asn Ser Glu Val Ser Lys Cys Leu His  
 65 70 75 80

Asn Leu Pro Ile Gly Gly Lys Ile Thr Ala Glu Met Lys Ser Lys Leu  
 85 90 95

Gly Lys Cys Leu Thr Lys Ser Ser Arg Ile Asp Gly Phe Gly Lys Ala  
 100 105 110

Ile Phe Phe Ser Trp Thr Leu Tyr Ser Thr Val Gly Tyr Gly Ser Leu  
 115 120 125

Tyr Pro His Ser Thr Leu Gly Arg Tyr Leu Thr Ile Phe Tyr Ser Leu  
 130 135 140

Leu Met Ile Pro Val Phe Ile Ala Phe Lys Phe Glu Phe Gly Thr Phe  
 145 150 155 160

Leu Ala His Phe Leu Val Val Val Ser Asn Arg Thr Arg Leu Ala Val  
 165 170 175

Lys Lys Ala Tyr Tyr Lys Leu Ser Gln Asn Pro Glu Asn Ala Glu Thr  
 180 185 190

Pro Ser Asn Ser Leu Gln His Asp Tyr Leu Ile Phe Leu Ser Ser Leu  
 195 200 205

Leu Leu Cys Ser Ile Ser Leu Leu Ser Ser Ser Ala Leu Phe Ser Ser  
 210 215 220  
 Ile Glu Asn Ile Ser Tyr Leu Ser Ser Val Tyr Phe Gly Ile Ile Thr  
 225 230 235 240  
 Met Phe Leu Ile Gly Ile Gly Asp Ile Val Pro Thr Asn Leu Val Trp  
 245 250 255  
 Phe Ser Gly Tyr Cys Met Leu Phe Leu Ile Ser Asp Val Leu Ser Asn  
 260 265 270  
 Gln Ile Phe Tyr Phe Cys Gln Ala Arg Val Arg Tyr Phe Phe His Ile  
 275 280 285  
 Leu Ala Arg Lys Ile Leu Leu Leu Arg Glu Glu Asp Asp Gly Phe Gln  
 290 295 300  
 Leu Glu Thr Thr Val Ser Leu Gln His Ile Pro Ile Ile Asn Ser Gln  
 305 310 315 320  
 Cys Met Pro Ser Leu Val Leu Asp Cys Glu Lys Glu Glu Leu Asp Asn  
 325 330 335  
 Asp Glu Lys Leu Ile Ser Ser Leu Thr Ser Thr  
 340 345

<210> 7  
 <211> 383  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: TWIK-1 homolog

<400> 7

Met Thr Val Ser Met Glu Glu Asn Ser Lys Ile Gln Met Leu Ser Ala  
 1 5 10 15  
 Thr Ser Lys Asp Lys Lys Val Ala Thr Asp Arg Ser Leu Leu Asn Lys  
 20 25 30  
 Tyr His Leu Gly Pro Leu Ala Leu His Thr Gly Leu Val Leu Ser Cys  
 35 40 45  
 Val Thr Tyr Ala Leu Gly Gly Ala Tyr Leu Phe Leu Ser Ile Glu His  
 50 55 60  
 Pro Glu Glu Leu Lys Arg Arg Glu Lys Ala Ile Arg Glu Phe Gln Asp  
 65 70 75 80  
 Leu Lys Gln Gln Phe Met Gly Asn Ile Thr Ser Gly Ile Glu Asn Ser  
 85 90 95  
 Glu Gln Ser Ile Glu Ile Tyr Thr Lys Lys Leu Ile Leu Met Leu Glu  
 100 105 110  
 Asp Ala His Asn Ala His Ala Phe Glu Tyr Phe Phe Leu Asn His Glu  
 115 120 125





Tyr Asp Lys Phe Gln Arg Ala Thr Ser Val Lys Arg Lys Leu Ser Ala  
340 345 350

Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Met Arg Thr  
355 360 365

Cys Leu  
370

<210> 9  
<211> 27  
<212> PRT  
<213> Homo sapiens

<220>  
<223> TWIK-1 P1

<400> 9

Phe Thr Ser Ala Leu Phe Phe Ala Ser Thr Val Leu Ser Thr Thr Gly  
1 5 10 15

Tyr Gly His Thr Val Pro Leu Ser Asp Gly Gly  
20 25

<210> 10  
<211> 27  
<212> PRT  
<213> Homo sapiens

<220>  
<223> TWIK-1 P2

<400> 10

Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser Thr Ile Gly  
1 5 10 15

Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn  
20 25

<210> 11  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

<220>  
<223> TOK-1 P2

<400> 11

Tyr Phe Asn Cys Ile Tyr Phe Cys Phe Leu Cys Leu Leu Thr Ile Gly  
1 5 10 15

Tyr Gly Asp Tyr Ala Pro Arg Thr Gly Ala Gly  
20 25

<210> 12  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> TOK-1 P1

<400> 12  
Tyr Gly Asn Ala Leu Tyr Phe Cys Thr Val Ser Leu Leu Thr Val Gly  
1 5 10 15

Leu Gly Asp Ile Leu Pro Lys Ser Val Gly Ala  
20 25

<210> 13  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

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<400> 13  
Tyr Trp Thr Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly  
1 5 10 15

Tyr Gly Asp Val Tyr Cys Glu Thr Val Leu Gly  
20 25

<210> 14  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>  
<223> Shaker

<400> 14  
Ile Pro Asp Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly  
1 5 10 15

Tyr Gly Asp Met Thr Pro Val Gly Phe Trp Gly  
20 25

<210> 15  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

<220>  
<223> Shab

<400> 15  
Ile Pro Glu Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly  
1 5 10 15

Tyr Gly Asp Ile Cys Pro Thr Thr Ala Leu Gly  
20 25

<210> 16  
<211> 27  
<212> PRT  
<213> Unknown

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<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

<220>  
<223> Shal

<400> 16  
Ile Pro Ala Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly  
1 5 10 15

Tyr Gly Asp Met Val Pro Glu Thr Ile Ala Gly  
20 25

<210> 17  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

<220>  
<223> Shaw

<400> 17  
Ile Pro Leu Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly  
1 5 10 15

Tyr Gly Asp Met Ala Pro Lys Thr Tyr Ile Gly  
20 25

<210> 18



<211> 27  
<212> PRT  
<213> Unknown

<220>

<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

<220>

<223> KAT1

<400> 18

Tyr Val Thr Ala Leu Tyr Trp Ser Ile Thr Thr Leu Thr Thr Thr Gly  
1 5 10 15

Tyr Gly Asp Phe His Ala Glu Asn Pro Arg Glu  
20 25

<210> 19

<211> 27

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

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<223> AKT1

<400> 19

Tyr Val Thr Ser Met Tyr Trp Ser Ile Thr Thr Leu Thr Thr Val Gly  
1 5 10 15

Tyr Gly Asp Ile His Pro Val Asn Thr Lys Glu  
20 25

<210> 20

<211> 27

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: P domain of  
representative K+ channel sequence

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<223> eag

<400> 20

Tyr Val Thr Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly  
1 5 10 15

Phe Gly Asn Val Ala Ala Glu Thr Asp Asn Glu  
20 25

<210> 21

<211> 27

<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

<220>  
<223> ROMK1

<400> 21  
Met Thr Ser Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly  
1 5 10 15

Tyr Gly Phe Arg Phe Val Thr Glu Gln Cys Ala  
20 25

<210> 22  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

<220>  
<223> IRK1

<400> 22  
Phe Thr Ala Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly  
1 5 10 15

Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys Pro  
20 25

<210> 23  
<211> 27  
<212> PRT  
<213> Unknown

<220>  
<223> Description of Unknown Organism: P domain of  
representative K<sup>+</sup> channel sequence

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<223> GIRK1

<400> 23  
Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly  
1 5 10 15

Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro  
20 25

<210> 24  
<211> 48  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: antisense  
oligonucleotide complementary to the partial  
mouse cDNA sequence of TASK

<400> 24

caccagcagg taggtgaagg tgcacacgat gagagccaac gtgcgcac

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